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1 IEGPTLRQWLAARA
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n immunoglobin molecule or its fragment no acid residues corresponding to at ary determining region (CDR) are ly active peptides e.g. a peptide (EDP) or thrombopoietin (TPO) mimetic, ts carboxy terminus. (I) has totropic activities, and can be used as fferentiation and maturation of	region in which amino acid ttion of the complementary with an erythropoietin or	aw M;		<pre>c peptide SEQ ID NO:2. ietin; antibody; CDR region; immunoglobin; antianaemic; oietic ceil; haematopoiesis.</pre>		Aaw09463 Thrombopo Aaw09468 Thrombopo Aaw3030 Thrombopo Aaw33034 Thrombopo Aaw33034 Thrombopo Aaw36774 Thrombopo Ad324843 AF 12505 Aay96515 Thrombopo Aab16962 TPO-mimet Aau26004 Human thr Aau26004 Human thr Abb72853 TPO mimet Abp51669 Thrombopo Aae18011 Human lig Abg71747 TPO recep Abr62907 Thrombopo Adc33697 Erythropo Adc33697 Erythropo Adc359652 Thrombopo Adc37293 Amino aci Adc72483 TPO mimet Adq16584 Agonist T			

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Matches 15
                     The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (EPO) mimetic. An immunoglobulin molecule of the inmunosuppressive activity, and may have a use in temunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow
                                                                                                                                                                                                                                                                                                                  New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with EPO mimetic or a TPO mimetic, useful for treating thrombocytopenia.
             transplantation,
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openia as a result of chemotherapy, be chronic diseases such as idiopathic
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etin; TPO; immunosuppressive;
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represents a TPO mimetic peptide.

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The present invention describes an immunoglobin molecule or its fragment CC (I) comprising a region where amino acid residues corresponding to at CC least a portion of the complementary determining region (CDR) are CC replaced or fused with biologically active peptides e.g. a peptide c mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, CC antianaemic, haemostatic and nephotropic activities, and can be used as stimulator of proliferation, differentiation and maturation of CC as stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with production. (I) which a region where amino acid residues corresponding to CC more of its CDRs fused with an EPO mimetic, is useful for increasing the CC production of the blood cells, where (I) is contacted with has one or conduction of the Diodo cells, where (I) is contacted with haematopoietic stem cells or their progenitors. (I) is useful for diagnostics or their progenitors. (I) is useful for diagnostics or conduction of their progenitors. (I) is useful for diagnostics or their progenitors. (I) is useful for diagnostics or conduction of the disclency in cell populations caused by disease, conducted by disease, conducted to ABQ733877 and ABP51669 to ABP51696 represent sequences used in
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                                                                                                                                                                                                                                                                                                                                               Claim 20; Fig 5; 113pp; English
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04-MAY-2001;
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least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoietic regils, and a stimulator of haematopoietic regils, and stimulator of proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with
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                                                                                                                                                    A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoletin or thrombopoetin mimetic.
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04-MAY-2001; 2001US-0288889P.
29-MAY-2001; 2001US-0294068P.
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The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful

Claim

Fig

5; 113pp; English.

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RESULT 10
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29-MAY-2001; 2001US-0294068P
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ning region are replaced or fused with an erythropoletin
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The present invention describes an immunoglobin molecule or its fra (1) comprising a region where amino acid residues corresponding to least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EBPO) or thrombopoletin (TPO) mime that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be us

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The present invention describes an immunoglobin molecule or its fra (I) comprising a region where amino acid residues corresponding to least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoletin (BPO) or thrombopoletin (TPO) min that is flanked with proline at its carboxy terminus. (I) has

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Example

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thrombopoetin mimetic.

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RESULT 11
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ID ABP51
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                                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 80; DB 5;
Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                Renshaw
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RESULT 12
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ADQ16621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in treating thrombocytopenia as a result of chemotherapy, bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                       New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wior a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin; complementarity determining erythropoietin; EPO; thrombopoietin; TPO; infimmunotherapy; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-460973/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-2002; 2002US-00307724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO mimetic peptide with random flanking residues SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18
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                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 31; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω,
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Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Renshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ng region; CDR; peptide mimetic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
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RESULT 13
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                                                                                                                              The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoletin (EPO) mimetic and a thrombopoletin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or creating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia.
                                                                                                                                                                                                                                                                                     New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transplantation, or of The present sequence residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive; immunotherapy; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18
                                                                                Seguence 18
                                                                                                                                                                                                                                                                                                                                                                               Bowdish
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ16619 standard; peptide;
                                                                                                         The present residues.
                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 39; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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DB; ADQ16620.
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     IEGPTLRQWLAARAP
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                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or chronic diseases such as idiopathic thrombocytopenia. ence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                            100.0%; Score 80; DI
100.0%; Pred. No. 2.1
tive 0; Mismatches
                                                                                                                    represents a TPO mimetic
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                                          2.1e-06;
                                                     DB 8;
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••
                                                                                                                    peptide with flanking
                                                    Length 18;
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RESULT 15
ADQ16646
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ADQ16621
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erythropoietin; l
immunotherapy; tl
                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoletin (EDR) mimetic and a thrombopoletin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ16621 standard; peptide; 18
immunoglobulin; complementarity determining region; CDR; peptide mimetic;
                                                         09-SEP-2004
                                                                                                               ADQ16646 standard; peptide; 18
                                                                                                                                                                                                                                                                                                Sequence 18
                                                                                                                                                                                                                                                                                                                             The present residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 41; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-2002; 2002US-00307724.
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                           TPO mimetic peptide SEQ ID NO:65.
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                                                                                                                                                                                     IEGPTLROWLAARAP 17
                                                                                                                                                                                                                                                                                                 Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide with random flanking residues SEQ ID NO:41.
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complementarity determining region; CDR; peptide mimetic; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                        100.0%;
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; Pred. No. 2.1e-06;
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                                                                                                                                                                                                                                                                    Length 18;
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                                                                                                                                                    The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoletin (EPO) mimetic and a thrombopoletin (TPO) mimetic. An immunoglobulin molecule of the invention has immunoglobulin molecule in unequal to the immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                              New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced without or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-460973/43.
N-PSDB; ADQ16645.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive; immunotherapy; thrombocytopenia.
                                                                                                                           Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 66; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowdish KS,
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w
                     1 IEGPTLRQWLAARAP
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IEGPTLROWLAARAP
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                                                                             100.0%;
 17
                                                              <u>,</u>
                                                                             Score 80; DB 8;
Pred. No. 2.1e-06;
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17, Appl
185, Appl
186, Appl
194, App
232, App
194, Appl
232, App
194, Appl
220, App
220, App
221, Appl
232, Appl
23

Sequence Sequence Sequence Sequence

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and is derived by analysis of the total score distribution.
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               77777777777777777777777777777
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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. (without alignments)
26.886 Million cell updates/sec
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            GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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                                        US-08-764-640-193
US-08-973-225-13
US-08-973-225-13
US-09-244-298A-13
US-09-244-298A-13
US-09-516-704-193
US-09-516-704-193
US-09-549-090-13
US-09-549-090-13
US-09-649-090-13
US-09-648-082B-26
US-09-428-082B-26
US-09-428-082B-32
US-09-428-092B-185
US-09-516-704-17
US-09-516-704-17
US-09-516-704-17
US-09-516-704-17
US-09-516-704-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
Sequence 13, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 185, Appl Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application (1) Sequence 13, Application (1) Sequence 13, Application (1) Sequence 13, Application (1) Sequence 14, Sequence 14, Sequence 15, Sequen
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATB: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION UNMBER: 36,392
REFERENCE/DOCKET NUMBER: 978.281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-08-764-640-13
         ; MOLECULE TYPE:
US-08-764-640-13
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APPLICANT:
APPLICANT:
APPLICANT:
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                LENGTH: 14 amazz
                                                                 TYPE: amino a STRANDEDNESS: TOPOLOGY: lin
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COUNTRY:
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Cwirla, Steven E.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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                                                                                                                                                          14 amino acids
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                                     peptide
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US-09-832-230A-185
US-08-764-640-194
US-08-764-640-232
US-08-764-640-232
US-08-973-225-194
US-08-973-225-20
US-08-973-225-220
US-09-244-298A-194
US-09-244-298A-194
US-09-244-298A-232
US-09-244-298A-232
US-09-216-704-194
US-09-516-704-194
US-09-516-704-232
US-09-549-090-18
US-09-549-090-18
US-09-549-090-18
US-09-549-090-194
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Regult No.

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RESULT 3
US-08-973-225-13
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US-08-764-640-193
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US-08-764-640-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Patent No. 5869451
; Patent No. 5869451 5837683
; GENERAL INFORMATION:
APPLICANT: Dower, William APPLICANT: Barrett, Rona
                      Sequence 13, Application US/08973225A
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY APPLICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
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CANT: Dower, William J.
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                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrett, Ronald W
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deprince, Randolph B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wagstrom, Christopher R. Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schatz, Peter J.
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                                                                                                                                                                                                                                                                                        91.2%; Score 73; DB 2;
100.0%; Pred. No. 2e-05;
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                                                                                                                                                                                                                                                                    <u>.</u>
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                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Box 13398
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2e-05;
hes 0; Indels
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                                                                                                                                                                                                                                                        0;
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; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Therefore The Control of th
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                                                                                                                                                                                                                                                                                                                                                    Sequence 193, Applicat:
Patent No. 6083913
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
              Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
THROMBOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Dower, William J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
Wrighton, PEPTIDES AND COMPOUNDS THAT BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLROWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                        Barrett, Ronald W. Cwirla, Steven E. Duffin, David J. Gates, Christian
                                                                                                                          Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
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Length 14; Indels

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TOPOLOGY: linear

HOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-08-973-225-193
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CLARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
TYPE: amino acid
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Best Local Similarity
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                                                                                                                                                                                                                                        APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                         ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
APPLICATION NUMBER:
                                                                                                                                     COUNTRY: U
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NUMBER: US/08/973,225A
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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COUNTRY: USA
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Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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100.0%; Pred. No. 2e-05;
Live 0; Mismatches
US/09/244,298A
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Patent No. 61
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                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REGISTRATION NUMBER: 36,392
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK:
TELECOMMUNICATION INFORMATION:
                                                                                                            REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PEPTIDES TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 27709
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CLASSIFICATION:
                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                          CITY: Research Triangle Park
             STRANDEDNESS:
                             TYPE: amino acid
                                                                                              TELEPHONE:
                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
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Hendren, Richard W.
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linear
                                                                                            919-248-1000
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                                                                             193:
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                                                                                                                                PK3281
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. 2e-05;
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US-09-516-704-193
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                                          RESULT 8
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BEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-516-704-13
                                                                                                                                                                                                                                                               COMPUTER: FIDDEY GLEAR
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION UNMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIGC, ROBERT T.
REGISTRATION NUMBER: 56,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
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Best Local S
Matches 14
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GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND
RECEPTOR
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14; Conservat
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                                                                                  IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NC
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Hendren, Richard W.
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100.0%; Pr
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f Score 73; DB
f; Pred. No. 2e-
0; Mismatches
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b; Pred. No. 2e-
0; Mismatches
                                                                                                                                                       DB 3;
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                                                                                                                                                                      Length 14;
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US-09-549-090-13
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                                                                                                                                                                                                           Sequence 13,
                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 193, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
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COUNTRY: USA
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Patent No. 6465430
GENERAL INFORMATION:
APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HTUbiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                             IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                   IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 14 amino acids
TYPE: amino acid
                                                                                                                                                                                                   Application US/09549090
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakts, Larry C.
Schatz, Peter J.
                                                                                                   Barrett, Ronald W.
Cwirla, Steven E.
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Hendren, Richard W.
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Balasubramanian, Palaniappan
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                                                                                                                                                                                                                                                                                                                                                                                             91.2%;
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                                                                                                                                                                                                                                                                                                                                                                          Score 73; DB 3; Length 14; Pred. No. 2e-05; O; Mismatches O; Indels
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TOPOLOGY: Intear
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MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-549-090-13
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US-09-549-090-193
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Best Local Similarity
Matches 14; Conserv
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK:
TELECOMMUNICATION INFORMATION: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS: Glaxo Wellcome
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                       Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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Barrett, Ronald W.
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                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CTTY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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ZIP: 27709
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                                                             COUNTRY: USA
ZIP: 27709
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                                                                                                    STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REET: Five Moore Drive, P.O. Box 13398
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                                                                                                                                                                                                                                                                                                                 Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                               Cwirla, Steven E. Duffin, David J.
                                                                                                                                                                                                                                                                                                 Schatz, Peter J
                                                                                                                                                                                                                                                                                                                                                                                                                  Barrett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.2%; Score 73; DB
100.0%; Pred. No. 2e-
tive 0; Mismatches
                                                                                                                                                                                                                     THROMBOPOIETIN RECEPTOR
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2e-05;
hes 0; Indels
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COUNTRY:

ZIP: 27709

COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/832,230A

FILING DATE: 10-Apr-2001

CLASSIFICATION: <Unknown>

AFTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

LENGTH: 14 amino acids
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-832-230A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-09-832-230A-13
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Itent No. 6506362
GENERAL INFORMATION:
GENERAL INFORMATION: William J. et al
APPLICANT: DOWER, William J. et al
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
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APPLICATION UNMBER: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/973,225
FILING DATE: <Unknown:
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, RODERT T
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
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SOFTWARE: PatentIn Release #1.0
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100.0%; Pred. No. 2e-05;
tive 0; Mismatches
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RESULT 12
US-09-832-230A-193
J. Sequence 193, Application US/09832230A
J. Patent No. 6506362
J. Patent No. FORMATION:
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US-09-428-0828-13
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MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-832-230A-193
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                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JAN
                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09428082B Patent No. 6660843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
CURRENT APPLICATION NUMBER: US/09/428,082B CURRENT FILING DATE: 1999-10-22
                                                                                              APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                           FILE REFERENCE: A-527
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/832,230A
FILLING DATE: 10-Apr-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT:INFORMATION:
NEARCH TOTALL TOTALL
NEARCH TOTALL
NEARCH
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEGPTLROWLAARA 14
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%; Pred. No. 2e-1
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RESULT 15
US-09-428-082B-29
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Best Local S
Matches 14
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                                                                                                                                             Sequence 29, Application US/09428082B Patent No. 6660843 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 14; Conserv
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GENERAL INFORMATION:
                                 APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FEIGE, ULRICH APPLICANT: LIU, CHUAN-FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (14)..(14)
OTHER INFORMATION: At position 14, amino acid linker to an identical sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHESTHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: TPO-MIMETIC PEPTIDE FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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milarity 100.0%; Pred. No.
Conservative 0; Mismatcl
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100.0%; Pred. No.
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2e-05;
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PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: TPO-MIMETIC PEPTIDE
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15) T. (16)
OTHER INFORMATION: Position 16 bromoscetyl group linked to sidechain
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14) T. (14)
OTHER INFORMATION: At position 14, amino acid linker attached N-to-C to Lys and to a
OTHER INFORMATION: nother linker and an identical sequence
US-09-428-0828-29
Search completed: December 20, 2004, 13:55:42 Job time : 38 secs
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                                                                                                                                                                                      Query Match 91.2%; Score 73; DB 4; Length 14; Best Local Similarity 100.0%; Pred. No. 2e-05; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                         1 IEGPTLRQWLAARA 14
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1 IEGPTLRQWLAARA 14
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Scoring table: Sequence: Title: Perfect score:

sequence

37, Appl 43, Appl 44, Appl 45, Appl 66, Appl 125, Appl 125, Appl 67, Appl 67, Appl 67, Appl 67, Appl 67, Appl 61, Appl 61, Appl 61, Appl 61, Appl 61, Appl 61, Appl 62, Appl 63, Appl 65, Appl 66, Appl 67, Appl 67, Appl 68, Appl 69, Appl 6

Run on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2-6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

5: /cgn2-6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2-6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

7: /cgn2-6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

8: /cgn2-6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

8: /cgn2-6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
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Match
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80
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/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
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 US-10-006-593-2

US-10-307-724-2

US-10-006-593-35

US-10-006-593-37

US-10-006-593-37

US-10-006-593-41

US-10-006-593-43

US-10-006-593-43

US-10-006-593-49

US-10-006-593-49

US-10-006-593-49

US-10-006-593-49

US-10-006-593-66

US-10-307-724-35
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                                                                                                                                                                                                                                                Description
Sequence 2, Appli
Sequence 2, Appli
Sequence 31, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 39, Appl
Sequence 41, Appl
Sequence 43, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 31, Appl
                                                                                                                                                                                                                            APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
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                                                                                                                                                            ; FEATURE: ; OTHER INFORMATION: TPO mimetic with flanking US-10-006-593-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-006-593-2
                                                                                         Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10006593
Publication No. US20030049683A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
                                                                                                                                                                                                             ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
15; Conserv
                                                        1 IEGPTLROWLAARAP 15
                       IEGPTLRQWLAARAP
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US-10-307-724-43
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US-10-307-724-43
US-10-307-724-66
US-10-307-724-130
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US-10-632-388-32
US-10-651-723-13
US-10-651-723-13
US-10-651-723-29
US-10-651-723-29
                                                                                         Score 80; DE
Pred. No. 1.3
0; Mismatches
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Sequence

Result

Score

Length

0

Gaps

rence 2, Application US/10307724

INFORMATION:

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                                                                                                            ; OTHER INFORMATION: TPO mimetic with flanking amino acids US-10-006-593-31
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                                        Matches
                                                         Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-12-05
PRIOR PEPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILING DATE: 2001-12-05
NUMBER DE SEO 11-12-05
                                                                                                                                                                                                                                  SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/10006593 Publication No. US20030049683A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/006,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -10-006-593-31
                                                                                                                                                       TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bowdish, Katherine S. APPLICANT: Frederickson, Shana APPLICANT: Renshaw, Mark
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TYPE: PRT
ORGANISM: artificial sequence
1 IEGPTLRQWLAARAP 15
                                                                                                                                                                                                                                                   PatentIn version 3.1
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15; Conserv
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                                      Conservative
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                                                   100.0%; Score 80; DB 14; 100.0%; Pred. No. 1.6e-05;
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Pred. No. 1.3e-05;
                                Mismatches
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                                                                     Length 18;
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                                Indels
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                          Gaps
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CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT ETLING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2011-05-29
UNUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3.7
                                                                                              ; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-37
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PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 35
LENGTH: 18
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Best Local Similarity
Matches 15; Conserva
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Query Match 100.0%; Score 80; DB 14; Best Local Similarity 100.0%; Pred. No. 1.6e-05; Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                       TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
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APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
                                                                                                                                                                                                       ENGTH:
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ORGANISM: artificial sequence
FEATURE:
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                                       DB 14; Length 18;
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; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-39
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR APPLICATION NUMBER: US 60/284,068
PRIOR FILING DATE: 2001-05-04
PRIOR PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
                                                                                        ; OTHER INFORMATION: TPO mimetic with flanking amino acids US-10-006-593-41
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Query Match 100.0%; Score 80; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
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APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
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                                                                                                                                TYPE: PRT ORGANISM: artificial sequence FEATURE:
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Pred. No.
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                                       Length 18;
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; TYPE: PRT; ORGANISM: artificial sequence; PEATURE: TYPOTHER INFORMATION: TPO mimetic with flanking amino acids US-10-006-593-43
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                                                               ; OTHER INFORMATION: TPO mimetic with flanking amino acids US-10-006-593-45
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US-10-006-593-45
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448;
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
                                                                                                         SEQ ID NO 45
LENGTH: 18
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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Query Match
Best Local Similarity
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APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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100.0%;
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Score 80;
Pred. No.
DB 14; Length 18
1.6e-05;
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; FEATURE:
; OTHER INFORMATION: TPO mimetic peptide with flanking sequence
US-10-006-593-66
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CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR PRIOR APPLICATION NUMBER: US 60/294,068
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           Query Match
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SOFTWARE: PatentIn version
SEQ ID NO 66
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
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APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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                                                                           TYPE: PRT
ORGANISM: artificial sequence
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
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PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
                                                                                                                                 LENGTH:
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lication No. US20030049683A1
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es 15; Conservation
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       100.0%;
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   Score 80;
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Pred. No. 1.6e-05;
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DB 14; Length 18,
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PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILLING DATE: 2000-12-05
PRIOR FILLING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILLING DATE: 2001-05-29
PRIOR FILLING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILLING DATE: 2001-12-05
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US-10-307-724-35
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                               SOFTWARE: Pate
SEQ ID NO 35
LENGTH: 18 -
TYPE: PRT
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CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR PILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-13-05
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US-10-307-724-31
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Publication No. US20030232972A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Matches 1
                                                                                                                   NUMBER OF SEQ ID NOS: 134
                                                                                                                                                                                                                                                                                                                            APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bowdish,
APPLICANT: Frederic
APPLICANT: Renshaw
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ORGANISM: artificial sequence
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APPLICANT: Frederickson,
APPLICANT: Renshaw, Mark
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ORGANISM: artificial sequence
FEATURE:
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                                                                                             PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Katherine S
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; Mismatches 0;
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APPLICANT: Bowdish, Katherine S.
APPLICANT: Prederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR APPLICATION NUMBER: US 60/284,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-05
PRIOR FILING DATE: 2001-05-07
PRIOR FILING DATE: 2001-05-07
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US-10-307-724-39
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; OTHER INFORMATION: TPO mimetic with flanking amino acids US-10-307-724-35
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OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-307-724-37
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PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 134
SOFTWARE: Patentin version 3.2
SEQ ID NO 37
LENGTH: 18
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Publication No. US20030232972A1
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ORGANISM: artificial sequence
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Pred. No. 1.6e-05;
); Mismatches 0;
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                                                  Query Match
Best Local S
Matches 15
                                                                                                                   SOFTWARE: PatentIn version 3.2
SEQ ID NO 39
LENGTH: 18
TYPE: PRT
ORGANIE:
PEATURE:
PEATURE:
POTHER INFORMATION: TPO mimetic with flanking amino acids
                                                    15;
                      1 IEGPTLROWLAARAP 15
                                                                Similarity
IEGPTLROWLAARAP 17
                                                    Conservative
                                                               100.0%; Score 80; DB 14; 100.0%; Pred. No. 1.6e-05;
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                                                     Mismatches
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Search completed: December 20, 2004, 14:06:44
Job time : 144 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being priand is derived by analysis of the total score distribution.
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                                                                      hypothetical prote
pol polyprotein -
peptide synthetase
probable phosphopa
probable phosphopa
probable phosphopa
hypothetical 21.8K
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probable glutathio
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glyceraldehyde-3-p
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ABC transporter, A
UTP-glucose-1-phos
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2,3-dihydroxybenzo
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probable membrane
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probable membrane protein YPO1203 [imported] - Yersinia pestis (strain CO92) (;Species: Yersinia pestis (c;Species: Yersinia yersinia pestis (c;Species: Yersinia yersinia pestis (c;Species: Yersinia y
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A36925
C;Species: Xanthobacter flavus
C;Species: Xanthobacter flavus
C;Species: Xanthobacter flavus
C;Species: Xanthobacter flavus
C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text_change 09-Jul-2004
C;Accession: A36925; S1378, S35408
R;Van den Bergh, E.R.E.; Dijkhuizen, L.; Meijer, W.G.
J. Bacteriol. 175, 6097-6104, 1993
A;Title: CbbR, a LysR-type transcriptional activator, is required for expre.
A;Reference number: A36925; MUID:94012468; PMID:8407781
A;Accession: A36925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A;Residues: 1-33 <VAN>
A;Residues: 1-30 <ANDEROT:P25545; EMBL:Z22705; NID:g297851; PIDN:CAA80406.1; PID:g581
A;Cross-references: UNIPROT:P25545; EMBL:Z22705; NID:g297851; PIDN:CAA80406.1; PID:g581
R;Meijer, W.G.; Arnberg, A.C.; Enequist, H.G.; Terpstra, P.; Lidstrom, M.E.; Dijkhuizen
Mol. Gen. Genet. 225, 320-330, 1991
A;Title: Identification and organization of carbon dioxide fixation genes in Xanthobact
A;Reference number: S13573; MUID:91172133; PMID:1900916
A;Accession: S13578
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AG0147
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C;Superfamily: transcription activator LysR-type
C;Keywords: DNA binding; transcription regulation
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A; Residues: 1-150 <MEI>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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AD2315
A81958
E81015
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B95325
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Pred. No. 1.5;
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probable permease
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probable protein k
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glyceraldehyde-3-
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Database

4 2 2 1

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Maximum Minimum

DB DB

eq eq

length:

2000000000

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Result

Score

Match Length

B

H A36925

SUMMARIES

Query

49

61.9

44

DAG0147 C87021 C87021 T24742 T27464 T37464 T37464 R89708 R899708 R8997

Title: Perfect score:

US-10-006-593-2 80

1 IEGPTLRQWLAARAP 15

Run on: OM protein -

protein search, using

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model

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

Br

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Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: C87021
                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-400 <S
                                                                                                                                                                                                                                                                                                                                   serine-threonine protein kinase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87021
C;Accession: C87021
R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler,
R;Cole, S.T.; Biglmeier, K.; Davkin, K.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.;
eam, M.A.; Rutherford, K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70601
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70601
                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: galU
C;Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
C;Keywords: nucleotidyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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C;Species: Mycobacterium tuberculosis
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A;Residues: 1-296 <KUR>
A;Crose-references: UNIPROT:Q8ZGS7; GB;AL590842;
C;Genetics:
A;Gene: YPO1203
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Best Local &
Matches
                                                                                                                                               Cross-references: UNIPROT:069568; GB:AL450380; NID:gl3092968;
                   Matches
                                      Query Match
Best Local
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                                                                                           Mycobacterium tuberculosis probable
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                                 57.5%;
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72.7%;
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                                                  Score 46;
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Pred. No. 5.3;
l; Mismatches
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Pred. No.
          Mismatches
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                                                    DB 2;
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3.5;
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            4.
                                                                                        serine/threonine-specific
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۲.
                                                Length 400;
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Holroyd,
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probable glutathione transferase (EC 2.5.1.18)
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-:
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A;Map position: 4
A;Introns: 45/1; 76/1; 111/3
C;Superfamily: glutathione transferase
                                                                                                                                                                                                 A; Gene: CESP: K08F4.11
                                                                                                                                                                                                                                    A; Cross-references: EMBL: Z68879;
A; Experimental source: clone K081
                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-200 <WIL>
                                                                                                                                                                                                                                                                                                                           R;Hembry, C. submitted to the EMBL Data A;Reference number: Z19746 A;Accession: T23485
                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein K08F4.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 C;Accession: T23485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Gene: GTG
F;388-415/Domain: DNA binding #status predicted <DNA>
F;405-415/Region: helix-turn-helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-436 <COR>
A;Cross references: UNIPROT:Q45293; EMBL:Z66534
A;Cross-references: UNIPROT:Q45293; EMBL:Z66534
A;Experimental source: ATCC 13869
A;Note: The authors translated the initiation codon TGT for residue
A;Note: The authors translated the codon ATT for residue 125 as Tyr
A;Note: the source is designated as Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 170, 91-94, 1996
A;Title: Cloning and characterization of an IS-like element
A;Reference number: JC4742; MUID:96200862; PMID:8621097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
JC4742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transposase - Corynebacterium glutamicum
C;Species: Corynebacterium glutamicum
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change
                                                                       Matches
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Best Local
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                               IEGPTLROWLAAR 13
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                                                                   Conservative
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                                                                                                                                                                                                                                      clone K08F4
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                                                                                     Score 44; Pred. No. 7
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Pred. No. 1:
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                                                                   Mismatches
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03-Dec-1999

#text_change 09-Jul-2004

GST3 -

Caenorhabditis elegans

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A;Gene: entE
A;Map position:
C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-368, 'ECRRKSTAAR', 379-536 <STA>
A; Residues: 1-368, 'ECRRKSTAAR', 379-536 <STA>
A; Cross-references: GB: M27490; EMBL:X15058; NID:g41345; E
R; Liu, J; Duncan, K; Walsh, C.T.
J Bacteriol. 171, 791-798, 1989
A; Title: Nucleotide sequence of a cluster of Escherichia
A; Reference number: A91904; MUID:89123155; PMID:2521622
A; Accession: A32047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-536 <BLAT>
A;Residues: 1-536 <BLAT>
A;Residues: 1-536 <BLAT>
A;Cross-references: UNIPROT:P10378; GB:AE000165; GB:U00096; NID:g1786808;
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
FERS Microbiol. Lett. 59, 15-19, 199
A;Title: Nucleotide sequence of the Escherichia coli entE gene.
A;Reference number: A48308; MUID:89290355; PMID:2525505
A;Note: in Mediine 89290355 this citation is erroneously given as volume 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Tawe, W.N.; Eschbach, M.L.; Walter, R.D.; Henkle-Duehrsen, K. submitted to the EMBL Data Library, June 1997
A;Description: Paraquat mediates differential gene expression in
                         A;Pathway: enterobactin biosynthesis
A;Note: this is one component of a membrane-bound multienzyme complex that catalyzes the for transport into the cell
                                                                                                                                                                                                                                                               A;Cross-references: GB:M24148; NID:g304949; PIDN:AAA16101.1; PID:g450380
C;Comment: The enzymatic steps in the condensation of L-serine and 2,3-dihydroxybenzoic
ty is based on its recognized homology with 4-commarate-CoA ligase and by analogy with t
C;Comment: The formation of 2,3-dihydroxybenzoyl-AMP has been observed. The rapid reacti
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                                                                                                                                                                                                                                                 carrier protein)
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A; Residues: 393-536 <LIU>
                                                                                                         A, Description: catalyzes the formation
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;Molecule type: mRNA
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8; Conserv
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4-coumarate-CoA ligase;
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                                                                                                                                                                                                                                                 to release AMP, has also been observed.
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Pred. No. 7.6;
2; Mismatches
acetate-CoA ligase homology
                                                                                                         of 2,3-dihydroxybenzoyl-[carrier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: acid-thiol ligase; enterobactin biosynthesis; membrane-associated complex F_i69-526/Domain: acetate-CoA ligase homology <ACL>
                                                                                                                                                                    A;Cross-references: UNIPROT:Q8XBV3; GB:BA000007; A;Experimental source: strain O157:H7, substrain
                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-536 <HAY>
                                                                                                                                                                                                                                                 DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99708
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A; Residues: 1-536 <STO>
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R;Perna, N.T.; Plun)
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                             IEGPTLROWLAARA 14
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Yasunaga, T.; Kuhara,
                                                                                                                       4-coumarate-CoA ligase; acetate-CoA
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ce: strain O157:H7, substrair
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57.1%;
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A.; Dimalanta,
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anta, E.;
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                                                                                                                                                                                                                                                                                                                            K.; Yokoyama,
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Potamousis,
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K.; Apodaca
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A;Residues: 1-2
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A;Experimental
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R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Jory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
                                                                   R;Miranda-Rios, J.; Morera, C.; Taboada, H.; Davalos, A.; Encarnacion, J. Bacteriol. 179, 6887-6893, 1997
A;Title: Expression of thiamin biosynthetic genes (thiCOGE) and product A;Reference number: Z22737; MUID:98037482; PMID:9371431
A;Accession: T44257
A;Status: preliminary; translated from GB/EMBL/DDBJ
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H83415
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H83962
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                A; Molecule type: DNA
A; Residues: 1-204 <MIR>
A; Cross-references: UNIPROT: 034294;
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A;Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Residues: 1-762 <STO>
                                                                                                                                                                                                                   Species: Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Cross-references: UNIPROT:Q912P9; GB:AE004610; GB:AE004091; NID:g9947825; PIDN:AAG0523
;Experimental source: strain PAO1
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Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                   Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004;Accession: T44257
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   source:
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Pred. No. 29;
2; Mismatches
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Pred. No.
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                    EMBL: AF004408; NID: g2627325; PIDN: AAC45975.1;
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A; Residues: 1-664 < KUR>
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A; Residues: 1-285 < COL>
A; Cross-references: UNII
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R;Fraser, C.M.; Nor:
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Best Local (
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C;Accession: G88994

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; ma, A.; Mizutani-Ui, Y.; Uchiyama, I.; Baba, T.; Inoue, R.; Kaito, C.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aur A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: G88994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  they, L.; netrus..., 1998
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, A;Title: Complete genome sequence of Treponema pallidum, A;Title: Complete A71250; MUID:98332770; PMID:9665876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Genome: plasmid b
C;Superfamily: thiE protein; thiamin-phosphate
C;Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                            protein kinase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable dimethyladenosine transferase (ksgA) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                A; Cross-references: UNIPROT: Q99UP8; A; Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown;
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se: strain Nichols
                    53.8%;
46.7%;
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Pred. No.
4.
                    Score 43;
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Pred. No. 15;
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L; Mismatches
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                                                                                                                                                       PIDN: BAB42315.1;
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2: uniprot_trembl:*
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IULT 2 AAS03241 AAS03241; 02-MAR-20 02-MAR-20 02-MAR-20 02-MAR-20 GalU GalU GALU OR M Mycobace Bacceria; Corynebac NCBI TaxI [1] [1] SEQUENCE STRAIN-BAI Li LI ABO SUBMitted EMBL; ABO	Query Mat Best Loca Matches	[1] SEQUENCE SEQUENCE STRAIN-k1 L., Bar Li L., Bar Submitted EMBL; AEO InterPro; Pfam; PFOO; Complete E SEQUENCE	05-JUL- 05-JUL- 05-JUL- GalU- Name=ga Mycobac Bacteri Bacteri Coryneb Mycobac		66666666666666666666666666666666666666
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                                                                                                        InterPro; IPROUDENT, 1.

Pfam; PF00126; HTH 1; 1.

Pfam; PF03466; LysR substrate; 1.

R PRINTS; PR00039; HTHLYSR.

JR PROSITE; PS50931; HTH LYSR; 1.

Activator; DNA-binding; Transcription regulation.

HTH 1ysR-type.

HTH 1ysR-type.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000847; HTH Lysr.
InterPro; IPR005119; Lysr subst.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z22705; CAA80406.1;
EMBL; X17252; -; NOT_ANNO:
PIR; A36925; A36925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and organization of carbon dioxide fixation genes Xanthobacter flavus H4-14.";
MOI. Gen. Genet. 225:320-330(1991).
-!- FUNCTION: Transcriptional activator for the cbb operon (cbbLS for RuBisCO and other Calvin cycle genes. Binds specifically two binding sites in the cbbR-cbbL intergenic region.
-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94012468; PubMed=8407781;
van den Bergh E., Ditknizen L., Meijer W.G.;
"CbbR, a LygR-type transcriptional activator, is re
expression of the autotrophic CO2 fixation enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
HTH-type transcriptional regulator cbbR (RuBisCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBBR_XANFL
P25545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hyphomicrobiaceae; Xanthobacter, NCBI_TaxID=281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meijer W.G., Arnberg A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91172133; PubMed=1900916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=H4-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=cbbR; Synonyms=cfxO;
Xanthobacter flavus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcriptional regulator).
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           Score 49.5; D
Pred. No. 7.2;
2; Mismatches
                                                                                                        HTH lysr-type.
H-T-H motif (By similarity).
, 9B375B4FB2D1EE73 CRC64;
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Q8Y015;
01-MAR-2002
01-MAR-2002
01-MAR-2002
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STRAIN=A3(2)
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SEQUENCE FROM 145;
STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Qualil M.A., Kieser H.,
Thomson N.B., James R.D., Chandra G., Chen C.W., Collins t
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth t
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor
Seeger K., Saunders D., Moodward J.R., Barrell B.G., Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Artiat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisen N., Claudel-Renard C., Cunnac S., Demange N Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum.", "Genome 15:497-502(2002).

EMBL; AL646062; CAD14761.1; ...

Complete proteome; Hypothetical protein.

Complete proteome; Hypothetical protein.
                  Hopwood D.A.;
"Complete genome sequence coelicolor A3(2).";
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Q9RKM5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative MerR family transcriptional regulator.
OrderedLocusNamms=SCO4102; ORFNames=SCD17.06c;
                                                                                                                                                                                                                                                                                                                                                                                                        Streptomycineae; Streptomycetaceae; CBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Name=RS04149; OrderedLocusNames=RSc1059;
Ralstonia solanacearum (Pseudomonas solan
Bacteria; Proteobacteria; Betaproteobact
Bactheria; Proteobacteria; Betaproteobact
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Howarth S.,
O'Neil S.,
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                                                                                                                      InterPro; IPRO00210; BTB POZ.
InterPro; IPRO00283; MATH.
Pfam; PP000651; BTB; 1.
Pfam; PP00917; MATH; 1.
SMART; SM00225; BTB; 1.
SMART; SM00225; BTB; 1.
SMART; SM00061; MATH; 1.
PROSITE; PS50097; BTB; 1.
PROSITE; PS50144; MATH; 1.
SEQUENCE 375 AA; 41043 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TERMBLrel. 25, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
OSUNBa0053K19 27 protein (OSUNBb0060B08.2 protein).
Name=OSUNBa0053K19.27; Synonyms=OSUNBb0060B08.2;
OTYZE SELLVE (Japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                           Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W., Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y., Han B.,
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000551; HTH MerR.
InterPro; IPR009061; Putativ_DNA_bind.
Pfam; PF00376; MerR; 1.
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SMART; SM00422; HTH MERR; 1.

PROSITE; PS50937; HTH MERR 2; 1.

Complete proteome; DNA-binding.

SEQUENCE 319 AA; 34841 MW; 11
                                                                                                                                                                                                                                                                                EMBL; AL606645; CAE03519.2; -.
EMBL; AL606669; CAE04739.1; -.
Gramene; Q7XPP6; -
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                                                                                                                                                                                                                                                                                                                                 "Sequence and analysis of rice chromosome 4.";
Nature 420:316-320(2002).
                                                                                                                                                                                                                                                                 GO; GO:0005515; F:protein binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                           ; Score 49; DB; Pred. No. 9.9; 1; Mismatches
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09L8D4;
01-OCT-2000
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Molnar I., Schupp T., Ono M., Zirkle R.E., Milnamow M.,
Nowak-Thompson B., Engel N., Toupet C., Stratmann A., Cyr D.D.,
Gorlach J., Mayo J.M., Hu A., Goff S., Schmid J., Ligon J.M.;
"The biosynthetic gene cluster for the microtubule-stabilizing open thilones A and B from Sorangium cellulosum So ce90.";
Chem. Biol. 7:97-109(2000).
EMBL, AP210843; AR26904.1; -.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-OCT-2003 (TrEMBLrel. 25, Last annotation update)
12-OCT-2003 (TrEMBLrel. 25, Last annotation update)
13-OCT-2000 (TrEMBLrel. 15, Created)
14-OCT-2000 (TrEMBLrel. 15, Created)
15-OCT-2000 (TrEMBLrel. 15, Created)
16-OCT-2000 (TrEMBLrel. 15, Last sequence update)
16-OCT-2000 (TrEMBLrel. 15, Las
                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the plant pathogen Ralstonia Nature 415:497-502(2002).

-!-SIMILARITY: Contains 1 HTH luxR-type DNA-bind EMBL; AL646085; CAD18730.1; -.
HSSP, P11470; IFSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demang Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
GO; GO:000562; C:intracellular; IEA.
GO; GO:0005700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009059; bi_resp_regltr_C.
InterPro; IPR000197; HTH_Fis.
InterPro; IPR0007197; HTH_LuxR.
Pfam; PF00196; GerE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01.MAR-2002 (TYEMBLYE1. 20, Created)
01.MAR-2002 (TYEMBLYE1. 20, Last sequence update)
01.MAR-2004 (TYEMBLYE1. 26, Last annotation update)
PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid megaplasmid.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
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NON TER 1
SEQUENCE 607 AA; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=RS02135; OrderedLocusNames=RSp1579
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10; Conserv
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Pred. No. 1
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RESULT 9
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Best Local &
Matches 10
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Best Loc
Matches
                                                                                                          Q8QUJ6;
Q8QUJ6;
01-JUN-2002
01-JUN-2002
01-JUN-2002
                 He J.G., De Chan S.M.;
                        SEQUENCE FROM N.A. MEDLINE=21874810; PubMe He J.G., Deng M., Weng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9WWZO;
Q1-NOV-1999
Q1-NOV-1999
Q1-MAR-2004
                                                            Infectious spleen and kidney Viruses; dsDNA viruses, no RN unclassified Iridoviridae. NCBI_TaxID=180170;
"Complete genome kidney necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas putida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01590; HTHFIS.
PRINTS; PR00038; HTHLUXR.
PRODOM; PD000307; HTH LUXR; 1.
SMART; SM00421; HTH LUXR; 1.
Complete proteome; DNA-binding;
SEQUENCE 252 AA; 27666 MW; 4
                                                                                                                                                                                                                                                                                    InterPro; IPR000345; CytC heme BS.
InterPro; IPR009056; CytoChrome c.
Pfam; PF06934; CTI; 1.
                                                                                                                                                                                                                                                                                                                                   Junker F., Ramos J.L.;
"Involvement of the cis/trans isomerase
Pseudomonas putida DOT-TIE.";
J. Bacteriol. 181:5693-5700(1999).
                                                                                                                                                                                                                                                                                                                EMBL; AF110738; AAD41252.1; -. InterPro; IPR010706; CTI.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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8; Conserv
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766 AA; 87058 MW; A4A0FC6C22
                                                                                                                                                                                                              EGPTLRQWLAARAP
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                                                                                                                    (TrEMBLrel.
                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                PRELIMINARY;
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       analysis of the mandarin fish
                         PubMed=11878882;
Weng S.P., Li Z.,
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71.4%;
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21,
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12,
26,
                                                                                 RNA
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Last sequence update)
Last annotation updat
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Pred. No. 9.8;
3; Mismatches
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                                                                                                                                                                                                                                       Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                         necrosis
                                                                                                                                                PRT;
                                                                               stage; Iridoviridae;
                                                                                                                                                                                                                                                                   A4A0FC6C22C301FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Plasmid; Transcription regulation. 483403EE326F7C2E CRC64;
                                                                                                                                                                                                                              Mismatches
                         Zhou
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       infectious
                        Long Q.X.,
                                                                                                                                                                                                                                                 Length 766;
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                       Wang X.Z.,
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Q8ZGS7
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   Query Match
Best Local S
Matches
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Best Local S
Matches 7
                                                            Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-KIM5 / Biovar Mediaevalis;

STRAIN-KIM5 / Biovar Mediaevalis;

MEDLINE-22137863; PubMed-12142430;

Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G. Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Fetherston J.D., Matson J.S., B
                                                                                                                                 EMBL;
EMBL;
PIR; A
GO; GC
                                                                                                                                                                                                      Yang R.;
Submitted (APR-2003) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CO-92 / Biovar Orientalis;

MEDLINS=21470413; PubMed=11586360; DOI=10.1038/35097083;

Parkhill J., Wren B. W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyehev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.",

Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8ZGS7 PRELIMINARY; PRT; 296 AA.
Q8ZGS7, Q74WE0; Q7CH89;
Q1-MAR-2002 (TTEMBLrel. 20, Created)
Q1-MAR-2002 (TTEMBLrel. 20, Last sequence update)
Q1-OCT-2004 (TTEMBLrel. 28, Last annotation update)
Putative membrane protein (Putative transmembrane protein (Putative transmembrane protein (Putative transmembrane protein)
                                                                                       Pfam; PF00892; DUF6;
                                                                                                                                                          EMBL; AJ414147; CAC90042.1;
EMBL; AE013900; AAM86536.1;
EMBL; AE017130; AAS61189.1;
                                                                                                                                                                                                                               STRAIN-91001 / Biovar Mediaevalis;
Song Y., Tong Z., Wang I., Han Y.,
Han Y., Pang X., Zhai J., Chen F.,
Ye C., Du Z., Lin W., Wang J., Yu
                                                                                                                                                                                                                                                                                                                     "Genome sequence of Yersinia pestis J. Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 291:126-139(2001).
EMBL; AF371960; AAL98838.1;
SEQUENCE 941 AA; 106703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yersinia pestis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae;
                                                                                                      [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=632;
                                                                                                               ; AG0147; AG0147.
GO:0016021; C:integral to
GO:0016020; C:membrane; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    581 VQGPTLAQWICSTA 594
   Similarity 9; Conser
                                                         proteome;
296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conservation
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                                                                                                      IPR000620; DUF6.
    Conservative
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                                                            Transmembrane
               58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yersinia.
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Score 47; DB
Pred. No. 17;
0; Mismatches
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Pred. No. 36;
4; Mismatches
                                                                                                                                  membrane; IEA
                                                          45947413DCD54CFF CRC64;
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                                                                                                                                                                                                                                              Zhang J., Pei
Qin H., Wang
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            DB
17;
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36;
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Vang J., Li
H., Wang J.,
   2
                            Length 296;
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                                                                                                                                                                                                                                                         Wang J.,
                                                                                                                                                                                                                                 Huang
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RESULT 13
Q80ZR
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OS Mus r
OC Euka;
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 RESULT 14
Q888B5
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Q888B5 PRELIMINARY;
Q888B5;
01-JUN-2003 (TrEMBLrel.
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01-JUN-2003 (TrEMBLrel. 24, Last
01-JUN-2003 (TrEMBLrel. 24, Last
Similar to RIKEN cDNA 2010110K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2003) to the EMBL/GenBank/DDBJ EMBL; AE017130; AAS61189.1; -. SEQUENCE 296 AA; 31378 MW; 45947413DCD54CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=91001 / Biovar Mediaevalis;
Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., I
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang Yang R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-2004 (TrEMBLrel.
24-MAR-2004 (TrEMBLrel.
04-MAY-2004 (TrEMBLrel
                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2003) to the
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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24-MAR-2004
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
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                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    BC048547; AAH48547.1;
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8; Conserv
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                                                                                                             GPLAREWLAASPP
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llarity 81.8%;
Conservative
                                  PRELIMINARY;
                                                                                                                                                                         Conservative
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61.5%;
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Pred. No. 13;
1; Mismatches
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Sciurognathi;
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gene (Fragment).
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Li S., Guo
J., Huang
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                                                                                                                                                                                                                                                                      STRAIN=GMI1000
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                Burkholderiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 167 AA;
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OBXY68 PRELIMINARY; PRT; 252 AA.

OBXY68; (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.

Name=RS03457; OrderedLocusNames=RSC1895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madugu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Delang W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L., White O., Fraser C.M., Collmer A.; "The complete genome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringae pv. tomato DC3000."; Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot SArlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Counnac S., Demang Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
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OrderedLocusNames=PSPTO1115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; Betaproteobacteria; Bur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21681879; PubMed=11823852;
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PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
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                                                                                                                                                                                                                                           "Genome sequence of the plant pathogen Ralstonia solanacearum.";
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Pred. No.
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                                                          DNA-dependent; IEA.
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DR Pfam; PF00196; GerE; 1.

DR PRINTS; PR00038; HTHLIUXR; 1.

DR PCODOM; PD000307; HTH LUXR; 1.

KW Complete proteome; DNA-binding; Transcription regulation.

SQ SEQUENCE 252 AA; 27945 MW; 17FD89DC6803EPBF CRC64;

Query Match

Best Local Similarity 46.7%; Pred. No. 21;

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 IEGPTLROWLARRAP 15

Db 76 IDTPLMRRWFATRSP 90

Search completed: December 20, 2004, 13:54:17

Job time: 192 secs
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